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PCT

## RAW SEQUENCE LISTING

DATE: 10/01/2002

PATENT APPLICATION: US/09/937,779

TIME: 10:39:55

Input Set : A:\937779sq

Output Set: N:\CRF4\10012002\I937779.raw

3 <110> APPLICANT: Dahlquist, Anders,  
 4 Stahl, Ulf  
 5 Lenman, Marit  
 6 Banas, Antoni  
 7 Ronne, Hans  
 8 Stymne, Sten

10 <120> TITLE OF INVENTION: A NEW CLASS OF ENZYMES IN THE BIOSYNTHETIC PATHWAY FOR THE  
 PRODUCTION OF

11 TRIACYLGLYCEROL AND RECOMBINANT DNA MOLECULES ENCODING THESE ENZYMES

13 <130> FILE REFERENCE: BASF-NAE-3377-99-Sept-2000

15 <140> CURRENT APPLICATION NUMBER: US 09/937,779

C--> 17 <141> CURRENT FILING DATE: 2002-06-07

17 <150> PRIOR APPLICATION NUMBER: PCT/EP 00/02701

18 <151> PRIOR FILING DATE: 2000-03-23

20 <160> NUMBER OF SEQ ID NOS: 31

22 <170> SOFTWARE: PatentIn Ver. 2.1

24 <210> SEQ ID NO: 1

25 <211> LENGTH: 1986

26 <212> TYPE: DNA

27 <213> ORGANISM: Saccharomyces cerevisiae

29 <220> FEATURE:

30 <221> NAME/KEY: CDS

31 <222> LOCATION: (1)..(1983)

33 <400> SEQUENCE: 1

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37	1 5 10 15	
39	gat gaa aac aat aaa ggg ggt tct gtt cat aac aag cga gag agc aga	96
40	Asp Glu Asn Asn Lys Gly Gly Ser Val His Asn Lys Arg Glu Ser Arg	
41	20 25 30	
43	aac cac att cat cat caa cag gga tta ggc cat aag aga aga agg ggt	144
44	Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly	
45	35 40 45	
47	att agt ggc agt gca aaa aga aat gag cgt ggc aaa gat ttc gac agg	192
48	Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg	
49	50 55 60	
51	aaa aga gac ggg aac ggt aga aaa cgt tgg aga gat tcc aga aga ctg	240
52	Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu	
53	65 70 75 80	
55	att ttc att ctt ggt gca ttc tta ggt gta ctt ttg ccg ttt agc ttt	288
56	Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe	
57	85 90 95	
59	ggc gct tat cat gtt cat aat agc gat agc gac ttg ttt gac aac ttt	336
60	Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe	

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61	100	105	110	
63	gta aat ttt gat tca ctt aaa gtg tat ttg gat gat tgg aaa gat gtt	384		
64	Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val			
65	115 120 125			
67	ctc cca caa ggt ata agt tcg ttt att gat gat att cag gct ggt aac	432		
68	Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn			
69	130 135 140			
71	tac tcc aca tct tct tta gat gat ctc agt gaa aat ttt gcc gtt ggt	480		
72	Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly			
73	145 150 155 160			
75	aaa caa ctc tta cgt gat tat aat atc gag gcc aaa cat cct gtt gta	528		
76	Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val			
77	165 170 175			
79	atg gtt cct ggt gtc att tct acg gga att gaa agc tgg gga gtt att	576		
80	Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile			
81	180 185 190			
83	gga gac gat gag tgc gat agt tct gcg cat ttt cgt aaa cgg ctg tgg	624		
84	Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp			
85	195 200 205			
87	gga agt ttt tac atg ctg aga aca atg gtt atg gat aaa gtt tgt tgg	672		
88	Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp			
89	210 215 220			
91	ttg aaa cat gta atg tta gat cct gaa aca ggt ctg gac cca ccg aac	720		
92	Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn			
93	225 230 235 240			
95	ttt acg cta cgt gca gca cag ggc ttc gaa tca act gat tat ttc atc	768		
96	Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile			
97	245 250 255			
99	gca ggg tat tgg att tgg aac aaa gtt ttc caa aat ctg gga gta att	816		
100	Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile			
101	260 265 270			
103	ggc tat gaa ccc aat aaa atg acg agt gct gcg tat gat tgg agg ctt	864		
104	Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu			
105	275 280 285			
107	gca tat tta gat cta gaa aga cgc gat agg tac ttt acg aag cta aag	912		
108	Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys			
109	290 295 300			
111	gaa caa atc gaa ctg ttt cat caa ttg agt ggt gaa aaa gtt tgt tta	960		
112	Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu			
113	305 310 315 320			
115	att gga cat tct atg ggt tct cag att atc ttt tac ttt atg aaa tgg	1008		
116	Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp			
117	325 330 335			
119	gtc gag gct gaa ggc cct ctt tac ggt aat ggt ggt cgt ggc tgg gtt	1056		
120	Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val			
121	340 345 350			
123	aac gaa cac ata gat tca ttc att aat gca gca ggg acg ctt ctg ggc	1104		
124	Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly			
125	355 360 365			

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127 gct cca aag gca gtt cca gct cta att agt ggt gaa atg aaa gat acc 1152
128 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
129 370 375 380
131 att caa tta aat acg tta gcc atg tat ggt ttg gaa aag ttc ttc tca 1200
132 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
133 385 390 395 400
135 aga att gag aga gta aaa atg tta caa acg tgg ggt ggt ata cca tca 1248
136 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
137 405 410 415
139 atg cta cca aag gga gaa gag gtc att tgg ggg gat atg aag tca tct 1296
140 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
141 420 425 430
143 tca gag gat gca ttg aat aac aac act gac aca tac ggc aat ttc att 1344
144 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
145 435 440 445
147 cga ttt gaa agg aat acg agc gat gct ttc aac aaa aat ttg aca atg 1392
148 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
149 450 455 460
151 aaa gac gcc att aac atg aca tta tcg ata tca cct gaa tgg ctc caa 1440
152 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
153 465 470 475 480
155 aga aga gta cat gag cag tac tcg ttc ggc tat tcc aag aat gaa gaa 1488
156 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
157 485 490 495
159 gag tta aga aaa aat gag cta cac cac aag cac tgg tcg aat cca atg 1536
160 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
161 500 505 510
163 gaa gta cca ctt cca gaa gct ccc cac atg aaa atc tat tgt ata tac 1584
164 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
165 515 520 525
167 ggg gtg aac aac cca act gaa agg gca tat gta tat aag gaa gag gat 1632
168 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
169 530 535 540
171 gac tcc tct gct ctg aat ttg acc atc gac tac gaa agc aag caa cct 1680
172 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
173 545 550 555 560
175 gta ttc ctc acc gag ggg gac gga acc gtt ccg ctc gtg gcg cat tca 1728
176 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
177 565 570 575
179 atg tgt cac aaa tgg gcc cag ggt gct tca ccg tac aac cct gcc gga 1776
180 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
181 580 585 590
183 att aac gtt act att gtg gaa atg aaa cac cag cca gat cga ttt gat 1824
184 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
185 595 600 605
187 ata cgt ggt gga gca aaa agc gcc gaa cac gta gac atc ctc ggc agc 1872
188 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
189 610 615 620
191 gcg gag ttg aac gat tac atc ttg aaa att gca agc ggt aat ggc gat 1920

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192 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
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195 ctc gtc gag cca cgc caa ttg tct aat ttg agc cag tgg gtt tct cag      1968
196 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
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199 atg ccc ttc cca atg taa                                          1986
200 Met Pro Phe Pro Met
201                      660
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204 <211> LENGTH: 661
205 <212> TYPE: PRT
206 <213> ORGANISM: Saccharomyces cerevisiae
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214                      20                      25                      30
216 Asn His Ile His His Gln Gln Gly Leu Gly His Lys Arg Arg Arg Gly
217                      35                      40                      45
219 Ile Ser Gly Ser Ala Lys Arg Asn Glu Arg Gly Lys Asp Phe Asp Arg
220                      50                      55                      60
222 Lys Arg Asp Gly Asn Gly Arg Lys Arg Trp Arg Asp Ser Arg Arg Leu
223 65                      70                      75                      80
225 Ile Phe Ile Leu Gly Ala Phe Leu Gly Val Leu Leu Pro Phe Ser Phe
226                      85                      90                      95
228 Gly Ala Tyr His Val His Asn Ser Asp Ser Asp Leu Phe Asp Asn Phe
229                      100                     105                     110
231 Val Asn Phe Asp Ser Leu Lys Val Tyr Leu Asp Asp Trp Lys Asp Val
232                      115                     120                     125
234 Leu Pro Gln Gly Ile Ser Ser Phe Ile Asp Asp Ile Gln Ala Gly Asn
235                      130                     135                     140
237 Tyr Ser Thr Ser Ser Leu Asp Asp Leu Ser Glu Asn Phe Ala Val Gly
238 145                      150                     155                     160
240 Lys Gln Leu Leu Arg Asp Tyr Asn Ile Glu Ala Lys His Pro Val Val
241                      165                     170                     175
243 Met Val Pro Gly Val Ile Ser Thr Gly Ile Glu Ser Trp Gly Val Ile
244                      180                     185                     190
246 Gly Asp Asp Glu Cys Asp Ser Ser Ala His Phe Arg Lys Arg Leu Trp
247                      195                     200                     205
249 Gly Ser Phe Tyr Met Leu Arg Thr Met Val Met Asp Lys Val Cys Trp
250                      210                     215                     220
252 Leu Lys His Val Met Leu Asp Pro Glu Thr Gly Leu Asp Pro Pro Asn
253 225                      230                     235                     240
255 Phe Thr Leu Arg Ala Ala Gln Gly Phe Glu Ser Thr Asp Tyr Phe Ile
256                      245                     250                     255
258 Ala Gly Tyr Trp Ile Trp Asn Lys Val Phe Gln Asn Leu Gly Val Ile
259                      260                     265                     270
261 Gly Tyr Glu Pro Asn Lys Met Thr Ser Ala Ala Tyr Asp Trp Arg Leu
262                      275                     280                     285

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264 Ala Tyr Leu Asp Leu Glu Arg Arg Asp Arg Tyr Phe Thr Lys Leu Lys
265      290      295      300
267 Glu Gln Ile Glu Leu Phe His Gln Leu Ser Gly Glu Lys Val Cys Leu
268 305      310      315      320
270 Ile Gly His Ser Met Gly Ser Gln Ile Ile Phe Tyr Phe Met Lys Trp
271      325      330      335
273 Val Glu Ala Glu Gly Pro Leu Tyr Gly Asn Gly Gly Arg Gly Trp Val
274      340      345      350
276 Asn Glu His Ile Asp Ser Phe Ile Asn Ala Ala Gly Thr Leu Leu Gly
277      355      360      365
279 Ala Pro Lys Ala Val Pro Ala Leu Ile Ser Gly Glu Met Lys Asp Thr
280      370      375      380
282 Ile Gln Leu Asn Thr Leu Ala Met Tyr Gly Leu Glu Lys Phe Phe Ser
283 385      390      395      400
285 Arg Ile Glu Arg Val Lys Met Leu Gln Thr Trp Gly Gly Ile Pro Ser
286      405      410      415
288 Met Leu Pro Lys Gly Glu Glu Val Ile Trp Gly Asp Met Lys Ser Ser
289      420      425      430
291 Ser Glu Asp Ala Leu Asn Asn Asn Thr Asp Thr Tyr Gly Asn Phe Ile
292      435      440      445
294 Arg Phe Glu Arg Asn Thr Ser Asp Ala Phe Asn Lys Asn Leu Thr Met
295      450      455      460
297 Lys Asp Ala Ile Asn Met Thr Leu Ser Ile Ser Pro Glu Trp Leu Gln
298 465      470      475      480
300 Arg Arg Val His Glu Gln Tyr Ser Phe Gly Tyr Ser Lys Asn Glu Glu
301      485      490      495
303 Glu Leu Arg Lys Asn Glu Leu His His Lys His Trp Ser Asn Pro Met
304      500      505      510
306 Glu Val Pro Leu Pro Glu Ala Pro His Met Lys Ile Tyr Cys Ile Tyr
307      515      520      525
309 Gly Val Asn Asn Pro Thr Glu Arg Ala Tyr Val Tyr Lys Glu Glu Asp
310      530      535      540
312 Asp Ser Ser Ala Leu Asn Leu Thr Ile Asp Tyr Glu Ser Lys Gln Pro
313 545      550      555      560
315 Val Phe Leu Thr Glu Gly Asp Gly Thr Val Pro Leu Val Ala His Ser
316      565      570      575
318 Met Cys His Lys Trp Ala Gln Gly Ala Ser Pro Tyr Asn Pro Ala Gly
319      580      585      590
321 Ile Asn Val Thr Ile Val Glu Met Lys His Gln Pro Asp Arg Phe Asp
322      595      600      605
324 Ile Arg Gly Gly Ala Lys Ser Ala Glu His Val Asp Ile Leu Gly Ser
325      610      615      620
327 Ala Glu Leu Asn Asp Tyr Ile Leu Lys Ile Ala Ser Gly Asn Gly Asp
328 625      630      635      640
330 Leu Val Glu Pro Arg Gln Leu Ser Asn Leu Ser Gln Trp Val Ser Gln
331      645      650      655
333 Met Pro Phe Pro Met
334      660
336 <210> SEQ ID NO: 3

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:7; N Pos. 601,627  
Seq#:9; N Pos. 15,45,83,103,107,112,210  
Seq#:25; N Pos. 240,385  
Seq#:25; Xaa Pos. 41,89  
Seq#:26; N Pos. 601,627  
Seq#:28; N Pos. 15,45,83,103,107,112,210